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Fig. 1a.1

GCGGCCTGGC TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC
Met Arg Ala Leu Ala Gln Arg Ser
-27 -25 -20

GAC CGG CGG CTG CTG CTG CTT GTT GTT TTG TCA GTA ATG ATT CTT GAG
Asp Arg Arg Leu Leu Leu Leu Val Val Leu Ser Val Met Ile Leu Glu
-15 -10 -5

ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT
Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser
1 5 10

CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG
His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met
15 20 25

GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT
Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser
30 35 40 45

GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG
Glu Gly Thr Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly
50 55 60

TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC
Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys
65 70 75

CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT
Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp
80 85 90

TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG
Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu
95 100 105

ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC
Thr Gln Ala Gly Glu Tyr Leu Leu His Ile Gln Ser Glu Arg Ala Asn
110 115 120 125

TAC ACA GTA CTG TTC ACA GTG AAT GTA AGA GAT ACA CAG CTG TAT GTG
Tyr Thr Val Leu Phe Thr Val Asn Val Arg Asp Thr Gln Leu Tyr Val
130 135 140

CTA AGG AGA CCT TAC TTT AGG AAG ATG GAA AAC CAG GAT GCA CTG CTC
Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu
145 150 155

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TGC ATC TCC GAG GGT GTT CCG GAG CCC ACT GTG GAG TGG GTG CTC TGC
Cys Ile Ser Glu Gly Val Pro Glu Pro Thr Val Glu Trp Val Leu Cys
160 165 170

AAG GAG GAA AAG GTA CTT CAT GAG TTG TTC GGA ACA GAC ATC AGA TGC
Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys
190 195 200 205

GAT	CTA	AAC	CAG	GCT	CCT	CAG	AGC	ACA	CTG	CCC	CAG	TTA	TTC	CTG	AAA
Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser	Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys
			225					230					235		

GGA TTC GGG CTC ACC TGG GAG CTG GAA GAC AAA GCC CTG GAG GAG GGC
Gly Phe Gly Leu Thr Trp Glu Leu Glu Asp Lys Ala Leu Glu Glu Gly
255 260 265

ATT	CTC	TTG	GCC	TTT	GTG	TCT	TCC	GTG	GGA	AGG	AAC	GAC	ACC	GGA	TAT
Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser	Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr
				290					295					300	

ATC CTA GAA AAA GGG TTT ATA AAC GCT ACC AGC TCG CAA GAA GAG TAT
Ile Leu Glu Lys Gly Phe Ile Asn Ala Thr Ser Ser Gln Glu Glu Tyr
320 325 330

GAA ATT GAC CCG TAC GAA AAG TTC TGC TTC TCA GTC AGG TTT AAA GCG
Glu Ile Asp Pro Tyr Glu Lys Phe Cys Phe Ser Val Arg Phe Lys Ala
335 340 345

Fig. 1a.3

TAC	CCA	CGA	ATC	CGA	TGC	ACG	TGG	ATC	TTC	TCT	CAA	GCC	TCA	TTT	CCT	
Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp	Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	
350					355					360					365	
TGT	GAA	CAG	AGA	GGC	CTG	GAG	GAT	GGG	TAC	AGC	ATA	TCT	AAA	TTT	TGC	
Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	
				370					375						380	
GAT	CAT	AAG	AAC	AAG	CCA	GGA	GAG	TAC	ATA	TTC	TAT	GCA	GAA	AAT	GAT	
Asp	His	Lys	Asn	Lys	Pro	Gly	Glu	Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	
			385					390					395			
GAC	GCC	CAG	TTC	ACC	AAA	ATG	TTC	ACG	CTG	AAT	ATA	AGA	AAG	AAA	CCT	
Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	
		400					405					410				
CAA	GTG	CTA	GCA	AAT	GCC	TCA	GCC	AGC	CAG	GCG	TCC	TGT	TCC	TCT	GAT	
Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala	Ser	Gln	Ala	Ser	Cys	Ser	Ser	Asp	
	415					420					425					
GGC	TAC	CCG	CTA	CCC	TCT	TGG	ACC	TGG	AAG	AAG	TGT	TCG	GAC	AAA	TCT	
Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	Lys	Lys	Cys	Ser	Asp	Lys	Ser	
430					435					440					445	
CCC	AAT	TGC	ACG	GAG	GAA	ATC	CCA	GAA	GGA	GTT	TGG	AAT	AAA	AAG	GCT	
Pro	Asn	Cys	Thr	Glu	Glu	Ile	Pro	Glu	Gly	Val	Trp	Asn	Lys	Lys	Ala	
				450					455					460		
AAC	AGA	AAA	GTG	TTT	GGC	CAG	TGG	GTG	TCG	AGC	AGT	ACT	CTA	AAT	ATG	
Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	Ser	Ser	Ser	Thr	Leu	Asn	Met	
			465				470						475			
AGT	GAG	GCC	GGG	AAA	GGG	CTT	CTG	GTC	AAA	TGC	TGT	GCG	TAC	AAT	TCT	
Ser	Glu	Ala	Gly	Lys	Gly	Leu	Leu	Val	Lys	Cys	Cys	Ala	Tyr	Asn	Ser	
		480					485					490				
ATG	GGC	ACG	TCT	TGC	GAA	ACC	ATC	TTT	TTA	AAC	TCA	CCA	GGC	CCC	TTC	
Met	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Phe	Leu	Asn	Ser	Pro	Gly	Pro	Phe	
	495					500					505					
CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCC	TTC	TAT	GCG	ACC	ATT	GGG	CTC	TGT	
Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	Tyr	Ala	Thr	Ile	Gly	Leu	Cys	
510					515					520					525	
CTC	CCC	TTC	ATT	GTT	GTT	CTC	ATT	GTG	TTG	ATC	TGC	CAC	AAA	TAC	AAA	
Leu	Pro	Phe	Ile	Val	Val	Leu	Ile	Val	Leu	Ile	Cys	His	Lys	Tyr	Lys	
				530					535					540		

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AAG CAA TTT AGG TAC GAG AGT CAG CTG CAG ATG ATC CAG GTG ACT GGC
Lys Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Ile Gln Val Thr Gly
545 550 555

GAC CTT AAG TGG GAG TTC CCG AGA GAG AAC TTA GAG TTT GGG AAG GTC
Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe Gly Lys Val
575 580 585

ATT AGT AAA ACG GGA GTC TCA ATT CAG GTG GCG GTG AAG ATG CTA AAA
Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys Met Leu Lys
610 615 620

ATG ATG ACC CAC CTG GGA CAC CAT GAC AAC ATC GTG AAT CTG CTG GGG
Met Met Thr His Leu Gly His His Asp Asn Ile Val Asn Leu Leu Gly
640 645 650

TAT GGT GAC CTC CTC AAC TAC CTA AGA AGT AAA AGA GAG AAG TTT CAC
Tyr Gly Asp Leu Leu Asn Tyr Leu Arg Ser Lys Arg Glu Lys Phe His
670 675 680 685

ACT TTC CAG GCA CAT TCA AAT TCC AGC ATG CCT GGT TCA CGA GAA GTT
Thr Phe Gln Ala His Ser Asn Ser Ser Met Pro Gly Ser Arg Glu Val
705 710 715

CAG TTA CAC CCG CCC TTG GAT CAG CTC TCA GGG TTC AAT GGG AAT TCA
Gln Leu His Pro Pro Leu Asp Gln Leu Ser Gly Phe Asn Gly Asn Ser
720 725 730

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ATT Ile	CAT His 735	TCT Ser	GAA Glu	GAT Asp	GAG Glu	ATT Ile 740	GAA Glu	TAT Tyr	GAA Glu	AAC Asn	CAG Gln 745	AAG Lys	AGG Arg	CTG Leu	GCA Ala
GAA Glu 750	GAA Glu	GAG Glu	GAG Glu	GAA Glu	GAT Asp 755	TTG Leu	AAC Asn	GTG Val	CTG Leu	ACG Thr 760	TTT Phe	GAA Glu	GAC Asp	CTC Leu	CTT Leu 765
TGC Cys	TTT Phe	GCG Ala	TAC Tyr	CAA Gln 770	GTG Val	GCC Ala	AAA Lys	GGC Gly	ATG Met 775	GAA Glu	TTC Phe	CTG Leu	GAG Glu	TTC Phe 780	AAG Lys
TCG Ser	TGT Cys	GTC Val	CAC His 785	AGA Arg	GAC Asp	CTG Leu	GCA Ala	GCC Ala 790	AGG Arg	AAT Asn	GTG Val	TTG Leu	GTC Val 795	ACC Thr	CAC His
GGG Gly	AAG Lys	GTG Val 800	GTG Val	AAG Lys	ATC Ile	TGT Cys	GAC Asp 805	TTT Phe	GGA Gly	CTG Leu	GCC Ala	CGA Arg 810	GAC Asp	ATC Ile	CTG Leu
AGC Ser 815	GAC Asp	TCC Ser	AGC Ser	TAC Tyr	GTC Val	GTC Val 820	AGG Arg	GGC Gly	AAC Asn	GCA Ala	CGG Arg 825	CTG Leu	CCG Pro	GTG Val	AAG Lys
TGG Trp 830	ATG Met	GCA Ala	CCC Pro	GAG Glu	AGC Ser 835	TTA Leu	TTT Phe	GAA Glu	GGG Gly	ATC Ile 840	TAC Tyr	ACA Thr	ATC Ile	AAG Lys	AGT Ser 845
GAC Asp	GTC Val	TGG Trp	TCC Ser	TAC Tyr 850	GGC Gly	ATC Ile	CTT Leu	CTC Leu	TGG Trp 855	GAG Glu	ATA Ile	TTT Phe	TCA Ser	CTG Leu 860	GGT Gly
GTG Val	AAC Asn	CCT Pro	TAC Tyr 865	CCT Pro	GGC Gly	ATT Ile	CCT Pro	GTC Val 870	GAC Asp	GCT Ala	AAC Asn	TTC Phe	TAT Tyr 875	AAA Lys	CTG Leu
ATT Ile	CAG Gln 880	AGT Ser	GGA Gly	TTT Phe	AAA Lys	ATG Met	GAG Glu 885	CAG Gln	CCA Pro	TTC Phe	TAT Tyr	GCC Ala 890	ACA Thr	GAA Glu	GGG Gly
ATA Ile 895	TAC Tyr	TTT Phe	GTA Val	ATG Met	CAA Gln	TCC Ser 900	TGC Cys	TGG Trp	GCT Ala	TTT Phe	GAC Asp 905	TCA Ser	AGG Arg	AAG Lys	CGG Arg

Fig. 1a.6

CCA TCC TTC CCC AAC CTG ACT TCA TTT TTA GGA TGT CAG CTG GCA GAG
 Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly Cys Gln Leu Ala Glu
 910 915 920 925

GCA GAA GAA GCA TGT ATC AGA ACA TCC ATC CAT CTA CCA AAA CAG GCG
 Ala Glu Glu Ala Cys Ile Arg Thr Ser Ile His Leu Pro Lys Gln Ala
 930 935 940

GCC CCT CAG CAG AGA GGC GGG CTC AGA GCC CAG TCG CCA CAG CGC CAG
 Ala Pro Gln Gln Arg Gly Gly Leu Arg Ala Gln Ser Pro Gln Arg Gln
 945 950 955

GTG AAG ATT CAC AGA GAA AGA AGT TAGCGAGGAG GCCTTGGACC CCGCCACCCT
 Val Lys Ile His Arg Glu Arg Ser
 960 965

AGCAGGCTGT AGACCGCAGA GCCAAGATTA GCCTCGCCTC TGAGGAAGCG CCCTACAGCG
 CGTTGCTTCG CTGGACTTTT CTCTAGATGC TGTCTGCCAT TACTCCAAAG TGACTTCTAT
 AAAATCAAAC CTCTCCTCGC ACAGGCGGGA GAGCCAATAA TGAGACTTGT TGGTGAGCCC
 GCCTACCCTG GGGGCCTTTC CACGAGCTTG AGGGGAAAGC CATGTATCTG AAATATAGTA
 TATTCTTGTA AATACGTGAA ACAAACCAAA CCCGTTTTTTT GCTAAGGGAA AGCTAAATAT
 GATTTTTTAAA AATCTATGTT TTAAAATACT ATGTAACTTT TTCATCTATT TAGTGATATA
 TTTTATGGAT GGAAATAAAC TTTCTACTGT AAAAAAAAAA AAAAAAAAAA AAAAAAA

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Fig. 1b.1

CGAGGCGGCA TCCGAGGGCT GGGCCGGCGC CCTGGGGGAC CCCGGGCTCC GGAGGCC

ATG CCG GCG TTG GCG CGC GAC GCG GGC ACC GTG CCG CTG CTC GTT GTT
Met Pro Ala Leu Ala Arg Asp Ala Gly Thr Val Pro Leu Leu Val Val
-27 -25 -20 -15

TTT TCT GCA ATG ATA TTT GGG ACT ATT ACA AAT CAA GAT CTG CCT GTG
Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
-10 -5 1 5

ATC AAG TGT GTT TTA ATC AAT CAT AAG AAC AAT GAT TCA TCA GTG GGG
Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
10 15 20

AAG TCA TCA TCA TAT CCC ATG GTA TCA GAA TCC CCG GAA GAC CTC GGG
Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
25 30 35

TGT GCG TTG AGA CCC CAG AGC TCA GGG ACA GTG TAC GAA GCT GCC GCT
Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
40 45 50

GTG GAA GTG GAT GTA TCT GCT TCC ATC ACA CTG CAA GTG CTG GTC GAT
Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
55 60 65

GCC CCA GGG AAC ATT TCC TGT CTC TGG GTC TTT AAG CAC AGC TCC CTG
Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
70 75 80 85

AAT TGC CAG CCA CAT TTT GAT TTA CAA AAC AGA GGA GTT GTT TCC ATG
Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
90 95 100

GTC ATT TTG AAA ATG ACA GAA ACC CAA GCT GGA GAA TAC CTA CTT TTT
Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
105 110 115

ATT CAG AGT GAA GCT ACC AAT TAC ACA ATA TTG TTT ACA GTG AGT ATA
Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
120 125 130

AGA AAT ACC CTG CTT TAC ACA TTA AGA AGA CCT TAC TTT AGA AAA ATG
Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
135 140 145

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Fig. 1b.2

GAA Glu 150	AAC Asn	CAG Gln	GAC Asp	GCC Ala	CTG Leu 155	GTC Val	TGC Cys	ATA Ile	TCT Ser	GAG Glu 160	AGC Ser	GTT Val	CCA Pro	GAG Glu 165	CCG Pro 165
ATC Ile	GTG Val	GAA Glu	TGG Trp	GTG Val 170	CTT Leu	TGC Cys	GAT Asp	TCA Ser	CAG Gln 175	GGG Gly	GAA Glu	AGC Ser	TGT Cys	AAA Lys 180	GAA Glu
GAA Glu	AGT Ser	CCA Pro	GCT Ala 185	GTT Val	GTT Val	AAA Lys	AAG Lys	GAG Glu 190	GAA Glu	AAA Lys	GTG Val	CTT Leu	CAT His 195	GAA Glu	TTA Leu
TTT Phe	GGG Gly	ACG Thr 200	GAC Asp	ATA Ile	AGG Arg	TGC Cys	TGT Cys 205	GCC Ala	AGA Arg	AAT Asn	GAA Glu	CTG Leu 210	GGC Gly	AGG Arg	GAA Glu
TGC Cys 215	ACC Thr	AGG Arg	CTG Leu	TTC Phe	ACA Thr	ATA Ile 220	GAT Asp	CTA Leu	AAT Asn	CAA Gln	ACT Thr 225	CCT Pro	CAG Gln	ACC Thr	ACA Thr
TTG Leu 230	CCA Pro	CAA Gln	TTA Leu	TTT Phe	CTT Leu 235	AAA Lys	GTA Val	GGG Gly	GAA Glu	CCC Pro 240	TTA Leu	TGG Trp	ATA Ile	AGG Arg	TGC Cys 245
AAA Lys	GCT Ala	GTT Val	CAT His 250	GTG Val	AAC Asn	CAT His	GGA Gly	TTC Phe	GGG Gly 255	CTC Leu	ACC Thr	TGG Trp	GAA Glu	TTA Leu 260	GAA Glu
AAC Asn	AAA Lys	GCA Ala	CTC Leu 265	GAG Glu	GAG Glu	GGC Gly	AAC Asn	TAC Tyr 270	TTT Phe	GAG Glu	ATG Met	AGT Ser	ACC Thr 275	TAT Tyr	TCA Ser
ACA Thr	AAC Asn	AGA Arg 280	ACT Thr	ATG Met	ATA Ile	CGG Arg	ATT Ile 285	CTG Leu	TTT Phe	GCT Ala	TTT Phe	GTA Val 290	TCA Ser	TCA Ser	GTG Val
GCA Ala 295	AGA Arg	AAC Asn	GAC Asp	ACC Thr	GGA Gly	TAC Tyr 300	TAC Tyr	ACT Thr	TGT Cys	TCC Ser	TCT Ser 305	TCA Ser	AAG Lys	CAT His	CCC Pro
AGT Ser 310	CAA Gln	TCA Ser	GCT Ala	TTG Leu	GTT Val 315	ACC Thr	ATC Ile	GTA Val	GGA Gly	AAG Lys 320	GGA Gly	TTT Phe	ATA Ile	AAT Asn	GCT Ala 325
ACC Thr	AAT Asn	TCA Ser	AGT Ser	GAA Glu 330	GAT Asp	TAT Tyr	GAA Glu	ATT Ile	GAC Asp 335	CAA Gln	TAT Tyr	GAA Glu	GAG Glu	TTT Phe 340	TGT Cys

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Fig. 1b.3

TTT	TCT	GTC	AGG	TTT	AAA	GCC	TAC	CCA	CAA	ATC	AGA	TGT	ACG	TGG	ACC	
Phe	Ser	Val	Arg	Phe	Lys	Ala	Tyr	Pro	Gln	Ile	Arg	Cys	Thr	Trp	Thr	
			345					350					355			
TTC	TCT	CGA	AAA	TCA	TTT	CCT	TGT	GAG	CAA	AAG	GGT	CTT	GAT	AAC	GGA	
Phe	Ser	Arg	Lys	Ser	Phe	Pro	Cys	Glu	Gln	Lys	Gly	Leu	Asp	Asn	Gly	
		360					365					370				
TAC	AGC	ATA	TCC	AAG	TTT	TGC	AAT	CAT	AAG	CAC	CAG	CCA	GGA	GAA	TAT	
Tyr	Ser	Ile	Ser	Lys	Phe	Cys	Asn	His	Lys	His	Gln	Pro	Gly	Glu	Tyr	
	375					380					385					
ATA	TTC	CAT	GCA	GAA	AAT	GAT	GAT	GCC	CAA	TTT	ACC	AAA	ATG	TTC	ACG	
Ile	Phe	His	Ala	Glu	Asn	Asp	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	
390					395					400					405	
CTG	AAT	ATA	AGA	AGG	AAA	CCT	CAA	GTG	CTC	GCA	GAA	GCA	TCG	GCA	AGT	
Leu	Asn	Ile	Arg	Arg	Lys	Pro	Gln	Val	Leu	Ala	Glu	Ala	Ser	Ala	Ser	
			410					415						420		
CAG	GCG	TCC	TGT	TTC	TCG	GAT	GGA	TAC	CCA	TTA	CCA	TCT	TGG	ACC	TGG	
Gln	Ala	Ser	Cys	Phe	Ser	Asp	Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	
			425				430						435			
AAG	AAG	TGT	TCA	GAC	AAG	TCT	CCC	AAC	TGC	ACA	GAA	GAG	ATC	ACA	GAA	
Lys	Lys	Cys	Ser	Asp	Lys	Ser	Pro	Asn	Cys	Thr	Glu	Glu	Ile	Thr	Glu	
		440					445					450				
GGA	GTC	TGG	AAT	AGA	AAG	GCT	AAC	AGA	AAA	GTG	TTT	GGA	CAG	TGG	GTG	
Gly	Val	Trp	Asn	Arg	Lys	Ala	Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	
	455					460					465					
TCG	AGC	AGT	ACT	CTA	AAC	ATG	AGT	GAA	GCC	ATA	AAA	GGG	TTC	CTG	GTC	
Ser	Ser	Ser	Thr	Leu	Asn	Met	Ser	Glu	Ala	Ile	Lys	Gly	Phe	Leu	Val	
470					475					480					485	
AAG	TGC	TGT	GCA	TAC	AAT	TCC	CTT	GGC	ACA	TCT	TGT	GAG	ACG	ATC	CTT	
Lys	Cys	Cys	Ala	Tyr	Asn	Ser	Leu	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Leu	
			490					495						500		
TTA	AAC	TCT	CCA	GGC	CCC	TTC	CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCA	TTC	
Leu	Asn	Ser	Pro	Gly	Pro	Phe	Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	
			505					510					515			
TAT	GCA	ACA	ATT	GGT	GTT	TGT	CTC	CTC	TTC	ATT	GTC	GTT	TTA	ACC	CTG	
Tyr	Ala	Thr	Ile	Gly	Val	Cys	Leu	Leu	Phe	Ile	Val	Val	Leu	Thr	Leu	
		520					525					530				

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Fig. 1b.4

CTA ATT TGT CAC AAG TAC AAA AAG CAA TTT AGG TAT GAA AGC CAG CTA
Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
535 540 545

CAG	ATG	GTA	CAG	GTG	ACC	GGC	TCC	TCA	GAT	AAT	GAG	TAC	TTC	TAC	GTT
Gln	Met	Val	Gln	Val	Thr	Gly	Ser	Ser	Asp	Asn	Glu	Tyr	Phe	Tyr	Val
550					555					560					565

GAT TTC AGA GAA TAT GAA TAT GAT CTC AAA TGG GAG TTT CCA AGA GAA
Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu
570 575 580

AAT TTA GAG TTT GGG AAG GTA CTA GGA TCA GGT GCT TTT GGA AAA GTG
Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val
585 590 595

ATG	AAC	GCA	ACA	GCT	TAT	GGA	ATT	AGC	AAA	ACA	GGA	GTC	TCA	ATC	CAG
Met	Asn	Ala	Thr	Ala	Tyr	Gly	Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln
		600					605					610			

GTT GCC GTC AAA ATG CTG AAA GAA AAA GCA GAC AGC TCT GAA AGA GAG
Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Ser Glu Arg Glu
615 620 625

GCA	CTC	ATG	TCA	GAA	CTC	AAG	ATG	ATG	ACC	CAG	CTG	GGA	AGC	CAC	GAG
Ala	Leu	Met	Ser	Glu	Leu	Lys	Met	Met	Thr	Gln	Leu	Gly	Ser	His	Glu
630					635					640					645

AAT ATT GTG AAC CTG CTG GGG GCG TGC ACA CTG TCA GGA CCA ATT TAC
Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Ile Tyr
650 655 660

TTG	ATT	TTT	GAA	TAC	TGT	TGC	TAT	GGT	GAT	CTT	CTC	AAC	TAT	CTA	AGA
Leu	Ile	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg
			665					670					675		

AGT AAA AGA GAA AAA TTT CAC AGG ACT TGG ACA GAG ATT TTC AAG GAA
Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu
680 685 690

CAC AAT TTC AGT TTT TAC CCC ACT TTC CAA TCA CAT CCA AAT TCC AGC
His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser
695 700 705

ATG	CCT	GGT	TCA	AGA	GAA	GTT	CAG	ATA	CAC	CCG	GAC	TCG	GAT	CAA	ATC
Met	Pro	Gly	Ser	Arg	Glu	Val	Gln	Ile	His	Pro	Asp	Ser	Asp	Gln	Ile
710					715					720					725

Fig. 1b.5

TCA	GGG	CTT	CAT	GGG	AAT	TCA	TTT	CAC	TCT	GAA	GAT	GAA	ATT	GAA	TAT	
Ser	Gly	Leu	His	Gly	Asn	Ser	Phe	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	
				730					735					740		
GAA	AAC	CAA	AAA	AGG	CTG	GAA	GAA	GAG	GAG	GAC	TTG	AAT	GTG	CTT	ACA	
Glu	Asn	Gln	Lys	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	
			745					750					755			
TTT	GAA	GAT	CTT	CTT	TGC	TTT	GCA	TAT	CAA	GTT	GCC	AAA	GGA	ATG	GAA	
Phe	Glu	Asp	Leu	Leu	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	
		760					765					770				
TTT	CTG	GAA	TTT	AAG	TCG	TGT	GTT	CAC	AGA	GAC	CTG	GCC	GCC	AGG	AAC	
Phe	Leu	Glu	Phe	Lys	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
	775					780					785					
GTG	CTT	GTC	ACC	CAC	GGG	AAA	GTG	GTG	AAG	ATA	TGT	GAC	TTT	GGA	TTG	
Val	Leu	Val	Thr	His	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	
790					795					800					805	
GCT	CGA	GAT	ATC	ATG	AGT	GAT	TCC	AAC	TAT	GTT	GTC	AGG	GGC	AAT	GCC	
Ala	Arg	Asp	Ile	Met	Ser	Asp	Ser	Asn	Tyr	Val	Val	Arg	Gly	Asn	Ala	
				810					815					820		
CGT	CTG	CCT	GTA	AAA	TGG	ATG	GCC	CCC	GAA	AGC	CTG	TTT	GAA	GGC	ATC	
Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	
			825					830					835			
TAC	ACC	ATT	AAG	AGT	GAT	GTC	TGG	TCA	TAT	GGA	ATA	TTA	CTG	TGG	GAA	
Tyr	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	
		840					845					850				
ATC	TTC	TCA	CTT	GGT	GTG	AAT	CCT	TAC	CCT	GGC	ATT	CCG	GTT	GAT	GCT	
Ile	Phe	Ser	Leu	Gly	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala	
	855					860					865					
AAC	TTC	TAC	AAA	CTG	ATT	CAA	AAT	GGA	TTT	AAA	ATG	GAT	CAG	CCA	TTT	
Asn	Phe	Tyr	Lys	Leu	Ile	Gln	Asn	Gly	Phe	Lys	Met	Asp	Gln	Pro	Phe	
870					875					880					885	
TAT	GCT	ACA	GAA	GAA	ATA	TAC	ATT	ATA	ATG	CAA	TCC	TGC	TGG	GCT	TTT	
Tyr	Ala	Thr	Glu	Glu	Ile	Tyr	Ile	Ile	Met	Gln	Ser	Cys	Trp	Ala	Phe	
				890					895					900		
GAC	TCA	AGG	AAA	CGG	CCA	TCC	TTC	CCT	AAT	TTG	ACT	TCG	TTT	TTA	GGA	
Asp	Ser	Arg	Lys	Arg	Pro	Ser	Phe	Pro	Asn	Leu	Thr	Ser	Phe	Leu	Gly	
			905					910					915			

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Fig. 1b.6

TGT CAG CTG GCA GAT GCA GAA GAA GCG ATG TAT CAG AAT GTG GAT GGC
 Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
 920 925 930

CGT GTT TCG GAA TGT CCT CAC ACC TAC CAA AAC AGG CGA CCT TTC AGC
 Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
 935 940 945

AGA GAG ATG GAT TTG GGG CTA CTC TCT CCG CAG GCT CAG GTC GAA GAT
 Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala Gln Val Glu Asp
 950 955 960 965

TCG TAGAGGAACA ATTTAGTTTT AAGGACTTCA TCCCTCCACC TATCCCTAAC
 Ser

AGGCTGTAGA TTACCAAAAC AAGATTAATT TCATCACTAA AAGAAAATCT ATTATCAACT
 GCTGCTTCAC CAGACTTTTC TCTAGAAGCC GTCTGCGTTT ACTCTTGTTT TCAAAGGGAC
 TTTTGTA AAA TCAAATCATC CTGTCACAAG GCAGGAGGAG CTGATAATGA ACTTTATTGG
 AGCATTGATC TGCATCCAAG GCCTTCTCAG GCCGGCTTGA GTGAATTGTG TACCTGAAGT
 ACAGTATATT CTTGTAAATA CATAAAACAA AAGCATTTTG CTAAGGAGAA GCTAATATGA
 TTTTTTAAGT CTATGTTTTA AAATAATATG TAAATTTTTTC AGCTATTTAG TGATATATTT
 TATGGGTGGG AATAAAATTT CTA CTACTACAGA AAAAAAAAAA AAAAAAAAAA AAAAA

TCG TAGAGGAACA ATTTAGTTTT AAGGACTTCA TCCCTCCACC TATCCCTAAC

Fig. 2.1

CTGTGTCCCG CAGCCGGATA ACCTGGCTGA CCCGATTCCG CGGACACCCG TGCAGCCGCG
 GCTGGAGCCA GGGCGCCGGT GCCCGCGCTC TCCCCGGTCT TGCCTGCGG GGGCCGATAC
 CGCCTCTGTG ACTTCTTTGC GGGCCAGGGA CGGAGAAGGA GTCTGTGCCT GAGAACTGG
 GCTCTGTGCC CAGGCGCGAG GTGCAGG ATG GAG AGC AAG GGC CTG CTA GCT
 Met Glu Ser Lys Gly Leu Leu Ala
 -19 -15

GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC GCC TCT GTG GGT TTG
 Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala Ser Val Gly Leu
 -10 -5 1 5

CCT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC ACA CAG AAA GAC ATA
 Pro Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr Gln Lys Asp Ile
 10 15 20

CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT ACT TGC AGG GGA CAG
 Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr Cys Arg Gly Gln
 25 30 35

CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG CGT GAT TCT GAG GAA
 Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg Asp Ser Glu Glu
 40 45 50

AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC AGT ATC TTC TGC AAA
 Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp Ser Ile Phe Cys Lys
 55 60 65

ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT ACT GGA GCC TAC AAG
 Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr Gly Ala Tyr Lys
 70 75 80 85

TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT GTT TAT GTC TAT GTT
 Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val Tyr Val Tyr Val
 90 95 100

CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC AGT GAC CAG CAT GGC
 Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp Gln His Gly
 105 110 115

ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT GTG GTG ATC CCC TGC
 Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val Val Ile Pro Cys
 120 125 130

CTGTGTCCCG CAGCCGGATA ACCTGGCTGA CCCGATTCCG CGGACACCCG TGCAGCCGCG

CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT TGC GCT AGG TAT CCA
Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys Ala Arg Tyr Pro
135 140 145

ATA	GGC	TTT	ACT	CTC	CCC	AGT	TAC	ATG	ATC	AGC	TAT	GCC	GGC	ATG	GTC
Ile	Gly	Phe	Thr	Leu	Pro	Ser	Tyr	Met	Ile	Ser	Tyr	Ala	Gly	Met	Val
				170					175					180	

ATA	GTT	GTG	GTT	GTA	GGA	TAT	AGG	ATT	TAT	GAT	GTG	ATT	CTG	AGC	CCC
Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	Val	Ile	Leu	Ser	Pro
		200					205					210			

ACA GCG AGA ACA GAG CTC AAT GTG GGG CTT GAT TTC ACC TGG CAC TCT
Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe Thr Trp His Ser
230 235 240 245

CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	AGC	ACC	TTG	ACA	ATA
Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	Ser	Thr	Leu	Thr	Ile
			265					270					275		

AGT GGA CGG ATG ATC AAG AGA AAT AGA ACA TTT GTC CGA GTT CAC ACA
Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe Val Arg Val His Thr
295 300 305

AAG CCT TTT ATT GCT TTC GGT AGT GGG ATG AAA TCT TTG GTG GAA GCC
Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys Ser Leu Val Glu Ala
310 315 320 325

Fig. 2.3

ACA GTG GGC AGT CAA GTC CGA ATC CCT GTG AAG TAT CTC AGT TAC CCA
 Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys Tyr Leu Ser Tyr Pro
 330 335 340

GCT CCT GAT ATC AAA TGG TAC AGA AAT GGA AGG CCC ATT GAG TCC AAC
 Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg Pro Ile Glu Ser Asn
 345 350 355

TAC ACA ATG ATT GTT GGC GAT GAA CTC ACC ATC ATG GAA GTG ACT GAA
 Tyr Thr Met Ile Val Gly Asp Glu Leu Thr Ile Met Glu Val Thr Glu
 360 365 370

AGA GAT GCA GGA AAC TAC ACG GTC ATC CTC ACC AAC CCC ATT TCA ATG
 Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr Asn Pro Ile Ser Met
 375 380 385

GAG AAA CAG AGC CAC ATG GTC TCT CTG GTT GTG AAT GTC CCA CCC CAG
 Glu Lys Gln Ser His Met Val Ser Leu Val Val Asn Val Pro Pro Gln
 390 395 400 405

ATC GGT GAG AAA GCC TTG ATC TCG CCT ATG GAT TCC TAC CAG TAT GGG
 Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp Ser Tyr Gln Tyr Gly
 410 415 420

ACC ATG CAG ACA TTG ACA TGC ACA GTC TAC GCC AAC CCT CCC CTG CAC
 Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala Asn Pro Pro Leu His
 425 430 435

CAC ATC CAG TGG TAC TGG CAG CTA GAA GAA GCC TGC TCC TAC AGA CCC
 His Ile Gln Trp Tyr Trp Gln Leu Glu Glu Ala Cys Ser Tyr Arg Pro
 440 445 450

GGC CAA ACA AGC CCG TAT GCT TGT AAA GAA TGG AGA CAC GTG GAG GAT
 Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp Arg His Val Glu Asp
 455 460 465

TTC CAG GGG GGA AAC AAG ATC GAA GTC ACC AAA AAC CAA TAT GCC CTG
 Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys Asn Gln Tyr Ala Leu
 470 475 480 485

ATT GAA GGA AAA AAC AAA ACT GTA AGT ACG CTG GTC ATC CAA GCT GCC
 Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val Ile Gln Ala Ala
 490 495 500

AAC GTG TCA GCG TTG TAC AAA TGT GAA GCC ATC AAC AAA GCG GGA CGA
 Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile Asn Lys Ala Gly Arg
 505 510 515

Fig. 2.4

GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	GGT	CCT	GAA	ATT	ACT	
Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	Gly	Pro	Glu	Ile	Thr	
		520					525					530				
GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	AGT	GTG	TCC	CTG	TTG	
Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Leu	
	535					540					545					
TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	ACG	TGG	TAC	AAG	CTT	
Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	
550					555					560					565	
GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	TCA	CTC	ACA	CCA	GTT	
Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	Ser	Leu	Thr	Pro	Val	
				570					575					580		
TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	GGC	ACC	ATG	TTT	TCT	
Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	Gly	Thr	Met	Phe	Ser	
			585					590					595			
AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	CAG	AAT	GCC	TCT	CTG	
Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	Gln	Asn	Ala	Ser	Leu	
		600					605					610				
CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	GAT	AAG	AAG	ACC	AAG	
Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	Asp	Lys	Lys	Thr	Lys	
	615					620					625					
AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	CTA	GAG	CGC	ATG	GCA	
Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	Leu	Glu	Arg	Met	Ala	
630				635						640					645	
CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	ACA	ACC	ATT	GGC	GAG	
Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	Thr	Thr	Ile	Gly	Glu	
				650					655					660		
ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	CCT	ACC	CCA	CAC	ATT	
Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	Pro	Thr	Pro	His	Ile	
			665					670					675			
ACA	TGG	TTC	AAA	GAC	AAC	GAG	ACC	CTG	GTA	GAA	GAT	TCA	GGC	ATT	GTA	
Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	
		680					685					690				
CTG	AGA	GAT	GGG	AAC	CGG	AAC	CTG	ACT	ATC	CGC	AGG	GTG	AGG	AAG	GAG	
Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	
	695					700					705					

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Fig. 2.5

GAT Asp 710	GGA Gly	GGC Gly	CTC Leu	TAC Tyr	ACC Thr 715	TGC Cys	CAG Gln	GCC Ala	TGC Cys	AAT Asn 720	GTC Val	CTT Leu	GGC Gly	TGT Cys	GCA Ala 725
AGA Arg	GCG Ala	GAG Glu	ACG Thr	CTC Leu 730	TTC Phe	ATA Ile	ATA Ile	GAA Glu	GGT Gly 735	GCC Ala	CAG Gln	GAA Glu	AAG Lys	ACC Thr 740	AAC Asn
TTG Leu	GAA Glu	GTC Val	ATT Ile 745	ATC Ile	CTC Leu	GTC Val	GGC Gly	ACT Thr 750	GCA Ala	GTG Val	ATT Ile	GCC Ala	ATG Met 755	TTC Phe	TTC Phe
TGG Trp	CTC Leu	CTT Leu 760	CTT Leu	GTC Val	ATT Ile	CTC Leu	GTA Val 765	CGG Arg	ACC Thr	GTT Val	AAG Lys	CGG Arg 770	GCC Ala	AAT Asn	GAA Glu
GGG Gly 775	GAA Glu	CTG Leu	AAG Lys	ACA Thr	GGC Gly	TAC Tyr 780	TTG Leu	TCT Ser	ATT Ile	GTC Val	ATG Met 785	GAT Asp	CCA Pro	GAT Asp	GAA Glu
TTG Leu 790	CCC Pro	TTG Leu	GAT Asp	GAG Glu	CGC Arg 795	TGT Cys	GAA Glu	CGC Arg	TTG Leu	CCT Pro 800	TAT Tyr	GAT Asp	GCC Ala	AGC Ser	AAG Lys 805
TGG Trp	GAA Glu	TTC Phe	CCC Pro	AGG Arg 810	GAC Asp	CGG Arg	CTG Leu	AAA Lys	CTA Leu 815	GGA Gly	AAA Lys	CCT Pro	CTT Leu	GGC Gly 820	CGC Arg
GGT Gly	GCC Ala	TTC Phe	GGC Gly 825	CAA Gln	GTG Val	ATT Ile	GAG Glu	GCA Ala 830	GAC Asp	GCT Ala	TTT Phe	GGA Gly 835	ATT Ile	GAC Asp	AAG Lys
ACA Thr	GCG Ala	ACT Thr 840	TGC Cys	AAA Lys	ACA Thr	GTA Val	GCC Ala 845	GTC Val	AAG Lys	ATG Met	TTG Leu	AAA Lys 850	GAA Glu	GGA Gly	GCA Ala
ACA Thr 855	CAC His	AGC Ser	GAG Glu	CAT His	CGA Arg	GCC Ala 860	CTC Leu	ATG Met	TCT Ser	GAA Glu	CTC Leu 865	AAG Lys	ATC Ile	CTC Leu	ATC Ile
CAC His 870	ATT Ile	GGT Gly	CAC His	CAT His	CTC Leu 875	AAT Asn	GTG Val	GTG Val	AAC Asn	CTC Leu 880	CTA Leu	GGC Gly	GCC Ala	TGC Cys	ACC Thr 885
AAG Lys	CCG Pro	GGA Gly	GGG Gly	CCT Pro 890	CTC Leu	ATG Met	GTG Val	ATT Ile	GTG Val 895	GAA Glu	TTC Phe	TCG Ser	AAG Lys	TTT Phe 900	GGA Gly

Fig. 2.6

AAC CTA TCA ACT TAC TTA CGG GGC AAG AGA AAT GAA TTT GTT CCC TAT
 Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu Phe Val Pro Tyr
 905 910 915

AAG AGC AAA GGG GCA CGC TTC CGC CAG GGC AAG GAC TAC GTT GGG GAG
 Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly Glu
 920 925 930

CTC TCC GTG GAT CTG AAA AGA CGC TTG GAC AGC ATC ACC AGC AGC CAG
 Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln
 935 940 945

AGC TCT GCC AGC TCA GGC TTT GTT GAG GAG AAA TCG CTC AGT GAT GTA
 Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp Val
 950 955 960 965

GAG GAA GAA GAA GCT TCT GAA GAA CTG TAC AAG GAC TTC CTG ACC TTG
 Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe Leu Thr Leu
 970 975 980

GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC
 Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe
 985 990 995

TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG GCA GCA CGA AAC ATT
 Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile
 1000 1005 1010

CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT GAC TTC GGC TTG GCC
 Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala
 1015 1020 1025

CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA AAA GGA GAT GCC CGA
 Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg
 1030 1035 1040 1045

CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT TTT GAC AGA GTA TAC
 Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr
 1050 1055 1060

ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG TTG CTC TGG GAA ATA
 Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 1065 1070 1075

TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC AAG ATT GAT GAA GAA
 Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu
 1080 1085 1090

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g. 2.7

TTT TGT AGG AGA TTG AAA GAA GGA ACT AGA ATG CGG GCT CCT GAC TAC
Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr
1095 1100 1105

ACT ACC CCA GAA ATG TAC CAG ACC ATG CTG GAC TGC TGG CAT GAG GAC
Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Glu Asp
1110 1115 1120 1125

CCC AAC CAG AGA CCC TCG TTT TCA GAG TTG GTG GAG CAT TTG GGA AAC
Pro Asn Gln Arg Pro Ser Phe Ser Glu Leu Val Glu His Leu Gly Asn
1130 1135 1140

CTC CTG CAA GCA AAT GCG CAG CAG GAT GGC AAA GAC TAT ATT GTT CTT
Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu
1145 1150 1155

CCA ATG TCA GAG ACA CTG AGC ATG GAA GAG GAT TCT GGA CTC TCC CTG
Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser Leu
1160 1165 1170

CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG GAA GTG TGC GAC CCC
Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu Val Cys Asp Pro
1175 1180 1185

AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAT TAT CTC CAG AAC
Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser His Tyr Leu Gln Asn
1190 1195 1200 1205

AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA ACA TTT GAA GAT ATC
Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile
1210 1215 1220

CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA GAT GAC AGC CAG ACA
Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Ser Gln Thr
1225 1230 1235

GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG AAA ACT CTG GAA GAC
Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp
1240 1245 1250

AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG ATG CCC AGT AAA AGC
Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met Met Pro Ser Lys Ser
1255 1260 1265

AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG ACC AGT GGC TAC CAG
Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln
1270 1275 1280 1285

CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG AGA GGT GCT GCT TAG
Pro Ala Pro Pro Pro Thr Pro Gly Asn His Glu Arg Gly Ala Ala
1335 1340 1345

ATTTTCAAGT	GTTGTTCTTT	CCACCACCCG	GAAGTAGCCA	CATTTGATTT	TCATTTTTTG
AGGAGGGACC	TCAGACTGCA	AGGAGCTTGT	CCTCAGGGCA	TTCCAGAGA	AGATGCCCAT
GACCCAAGAA	TGTGTTGACT	CTACTCTCTT	TTCCATT CAT	TTAAAAGTCC	TATATAATGT
GCCCTGCTGT	GGTCTCACTA	CCAGTTAAAG	CAAAAGACTT	TCAAACACGT	GGACTCTGTC
CTCCAAGAAG	TGGCAACGGC	ACCTCTGTGA	AACTGGATCG	AATGGGCAAT	GCTTTGTGTG
TTGAGGATGG	GTGAGATGTC	CCAGGGCCGA	GTCTGTCTAC	CTTGAGGGCT	TTGTGGAGGA
TGCGGCTATG	AGCCAAGTGT	TAAGTGTGGG	ATGTGGACTG	GGAGGAAGGA	AGGCGCAAGC
CGTCCGGAGA	GCGGTTGGAG	CCTGCAGATG	CATTGTGCTG	GCTCTGGTGG	AGGTGGGCTT
GTGGCCTGTC	AGGAAACGCA	AAGGCGGCCG	GCAGGGTTTG	GTTTTGGAAG	GTTTGC GTGC
TCTTCACAGT	CGGGTTACAG	GCGAGTTCCC	TGTGGCGTTT	CCTACTCCTA	ATGAGAGTTC
CTTCCGGACT	CTTACGTGTC	TCCTGGCCTG	GCCCCAGGAA	GGAAATGATG	CAGCTTGCTC
CTTCCTCATC	TCTCAGGCTG	TGCCTTAATT	CAGAACACCA	AAAGAGAGGA	ACGTCGGCAG
AGGCTCCTGA	CGGGGCCGAA	GAATTGTGAG	AACAGAACAG	AAACTCAGGG	TTTCTGCTGG
GTGGAGACCC	ACGTGGCGCC	CTGGTGGCAG	GTCTGAGGGT	TCTCTGTCAA	GTGGCGGTAA
AGGCTCAGGC	TGGTGTTCCT	CCTCTATCTC	CACTCCTGTC	AGGCCCCCAA	GTCCTCAGTA
TTTTAGCTTT	GTGGCTTCCT	GATGGCAGAA	AAATCTTAAT	TGGTTGGTTT	GCTCTCCAGA

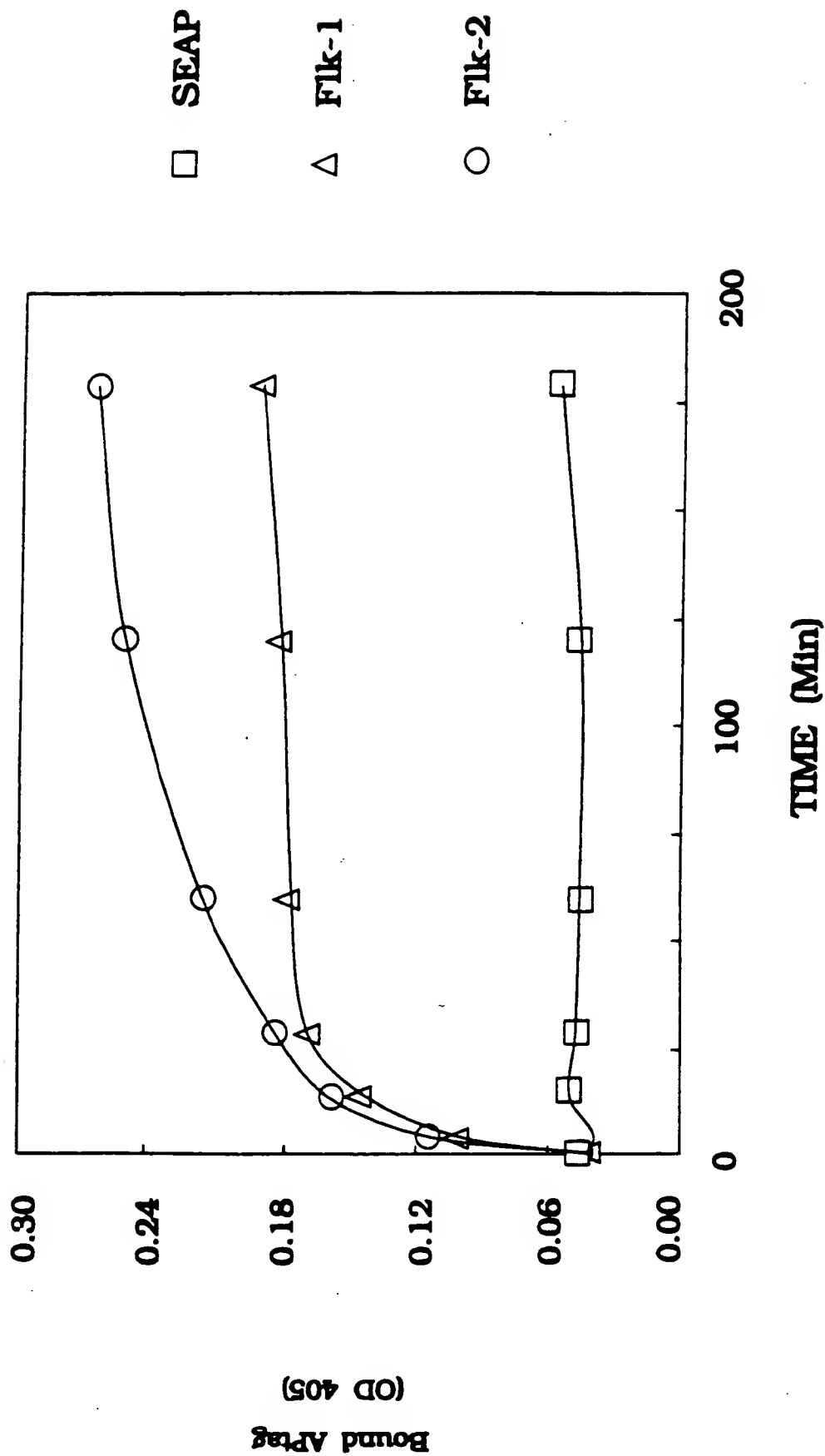
Fig. 2.9

TAATCACTAG CCAGATTTTCG AAATTACTTT TTAGCCGAGG TTATGATAAC ATCTACTGTA
TCCTTTAGAA TTTTAACCTA TAAAACTATG TCTACTGGTT TCTGCCTGTG TGCTTATGTT
AAAAAAAAAA AAAAA

[illegible]

1/1

FIGURE 3



1/1

FIGURE 4

